

WEST Search History

DATE: Wednesday, April 02, 2003

Set Name Query

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Hit Count Set Name result set

DB=USPT,PGPB,DWPI; THES=ASSIGNEE; PLUR=YES; OP=OR

L15	power-christine-a.in.	3	L15
L14	k5-5 and chemokine	1	L14
L13	powers-christine-a.in.	0	L13
L12	L10 and (@RLAD<19990115 or @PD<19990115)	9	L12
L11	L10 not L7	58	L11
L10	L9 and L3	63	L10
L9	(CC-CKR-4 or CKR4 or CMKBR4 or ChemR13 or HGCN:14099 or k5-5 or CCL17 or CTACK or ck.beta-13) and chemokine	106	L9
L8	L1 same antibody	38	L8
L7	L6 and (@RLAD<19990115 or @PD<19990115)	31	L7
L6	L5 and L3	122	L6
L5	CCR4 or TARC or MDC	1712	L5
L4	L3 and L1	81	L4
L3	atopic adj1 dermatitis	6430	L3
L2	Butcher-eugene-c.in.	12	L2
L1	CCR4	208	L1

END OF SEARCH HISTORY



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GeneCard for uncharacterized CCR4
GC03U990019

Approved UCL/HGNC/HUGO Human Gene Nomenclature database symbol
CCR4 (chemokine (C-C motif) receptor 4)

**Aliases and
Additional
Descriptions**
(According to GDB,
HUGO, and/or
SWISS-PROT)

- CC-CKR-4
- CKR4
- CMKBR4
- ChemR13
- HGCN:14099
- k5-5
- chemokine (C-C motif) receptor 4
- C-C chemokine receptor type 4 (C-C CKR-4) (CC-CKR-4) (CCR-4) (CCR4) (K5-5).

**Chromosomal
Location**
(According to
UDB/GeneLoc and/or
HUGO, and/or
LocusLink,
Genomic Views
According to UCSC
and Ensembl)

Chromosome: 3 UDB/GeneLoc gene densities

LocusLink cytogenetic band: 3p24 **Ensembl cytogenetic band:**

Unified DataBase (GeneLoc) location for GC03U990019: (about GC identifiers)

Start: unknown bp from pter

End: unknown bp from pter

Size: unknown bases

Orientation: unknown strand

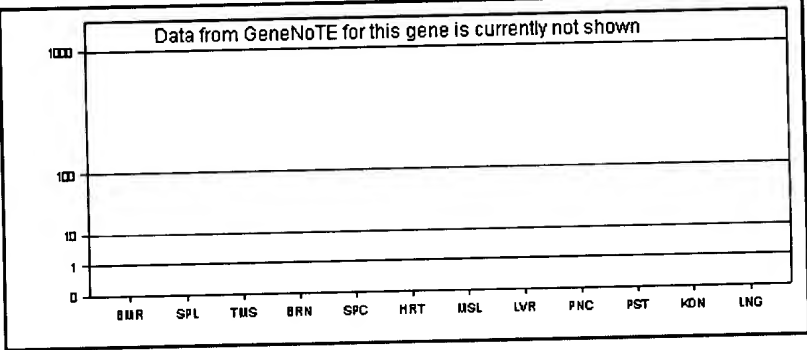
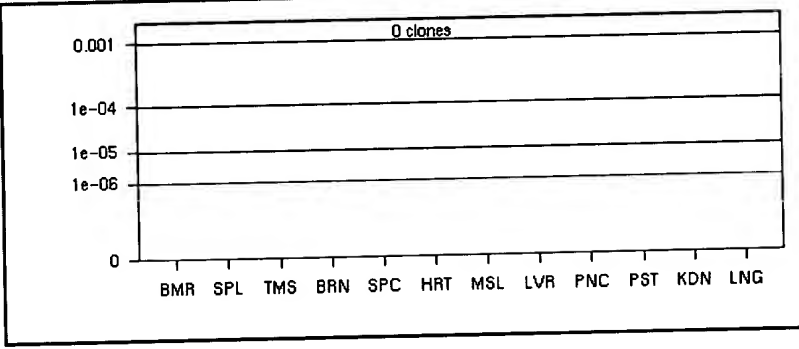
Unified DataBase (version 2.5) coordinate (from pter): 34.316 mega bases

Genomic View:
UCSC Golden Path

Proteins
(According to
SWISS-PROT and/or
MIPS)

CKR4 HUMAN

- **Size:** 360 amino acids; 41402 Da
- **Function:** HIGH AFFINITY RECEPTOR FOR THE C-C TYPE CHEMOKINES TARC/SCYA22. THE ACTIVITY OF THIS RECEPTOR IS MEDIATED BY G(I) PROTEINS WHICH ACTIVATE PHOSPHATIDYLINOSITOL-CALCIUM SECOND MESSENGER SYSTEM. CAN FUNCTION AS A CHEMOATTRACTANT RECEPTOR ON CIRCULATING MEMORY LYMPHOCYTES AND AS A CORECEPTOR FOR SOME PRIMARY HIV-2 CNS, COULD MEDIATE HIPPOCAMPAL-NEURON SURVIVAL.
- **Subcellular location:** Integral membrane protein.
- **Tissue specificity:** PREDOMINANTLY EXPRESSED IN THE THYMUS, IN PERIPHERAL BLOOD LEUKOCYTES, INCLUDING T CELLS, MOSTLY CD4+ CELLS, AND BASOPHILS, AND IN PLATELETS. DETECTED ALSO IN MACROPHAGES, IL-2-ACTIVATED T CELLS, AND SKIN-HOMING MEMORY T CELLS, MOSTLY THE ONES EXPRESSING THE CUTANEOUS LYMPHOCYTE ANTIGEN (CLA). EXPRESSED IN BRAIN MICROVASCULAR AND CORONARY ARTERY ENDOTHELIAL CELLS.
- **Ptm:** IN NATURAL KILLER CELLS, SCYA22 BINDING INDUCES PHOSPHORYLATION OF SER/THR RESIDUES, MOST PROBABLY BY BETA-ADRENERGIC RECEPTOR KINASES 1 AND 2.
- **Similarity:** BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.

	REFSEQ proteins: NP_005499.1																										
Protein Domains/ Families/Ontologies (According to InterPro, GO, and/or BLOCKS)	InterPro Domains and Families: IPR000276; GPCR_Rhodpsn Graphical View of Domain Structure for SP Entry P51679 Blocks protein family: IPB000276 Rhodopsin-like GPCR superfamily																										
Sequences (GenBank/EMBL/DBJ Accessions According to Unigene or GenBank , RefSeq According to LocusLink , Assembly According to MIPS and/or DOTS)	REFSEQ mRNAs: NM_005508.1 Additional Gene/cDNA sequence: AB023888.1 AB023889.1 AB023890.1 AB023891.1 AB023892.1 X85740 X85740.1 DOTS assembly: DT.40117006 Unigene Cluster for CCR4: (Build 155 Homo sapiens; Sep 23 2002) chemokine (C-C motif) receptor 4 Hs.184926 Unigene Representative Sequence: NM_005508																										
Expression in Human Tissues (According to proprietary W.I.S DNA array results (GeneNoTE), UniGene and/or SOURCE)	CCR4 expression in normal human tissues based on proprietary W.I.S DNA array (GeneNoTE)  <ul style="list-style-type: none"><input checked="" type="checkbox"/> Immune System<input checked="" type="checkbox"/> Nervous System<input type="checkbox"/> Muscle<input checked="" type="checkbox"/> Secretory Glands<input checked="" type="checkbox"/> Other<input type="checkbox"/> Min-max range for CCR4 expression in normal human tissues based on quantifying ESTs from various tissue clusters (Build 155 Homo sapiens).  <table><thead><tr><th colspan="2">Tissue</th></tr></thead><tbody><tr><td>BMR</td><td>Bone marrow</td></tr><tr><td>SPL</td><td>Spleen</td></tr><tr><td>TMS</td><td>Thymus</td></tr><tr><td>BRN</td><td>Brain</td></tr><tr><td>SPC</td><td>Spinal cord</td></tr><tr><td></td><td>Heart</td></tr><tr><td></td><td>Skeletal muscle</td></tr><tr><td>LVR</td><td>Liver</td></tr><tr><td>PNC</td><td>Pancreas</td></tr><tr><td>PST</td><td>Prostate</td></tr><tr><td>KDN</td><td>Kidney</td></tr><tr><td>LNG</td><td>Lung</td></tr></tbody></table> SOURCE GeneReport for Unigene cluster Hs.184926 Homologues:	Tissue		BMR	Bone marrow	SPL	Spleen	TMS	Thymus	BRN	Brain	SPC	Spinal cord		Heart		Skeletal muscle	LVR	Liver	PNC	Pancreas	PST	Prostate	KDN	Kidney	LNG	Lung
Tissue																											
BMR	Bone marrow																										
SPL	Spleen																										
TMS	Thymus																										
BRN	Brain																										
SPC	Spinal cord																										
	Heart																										
	Skeletal muscle																										
LVR	Liver																										
PNC	Pancreas																										
PST	Prostate																										
KDN	Kidney																										
LNG	Lung																										

Similar Genes in Other Organisms (According to MGD Oct 18 2002 , Stony Brook C.elegans-H.sapiens Alignment Database and/or euGenes)	<table><tr><td></td><td>gene</td><td>locus</td><td>description</td><td>%similarity to human</td></tr><tr><td>mouse (MGD)</td><td>Ccr4</td><td>9 (61.00 cM)</td><td>chemokine (C-C motif) receptor 4</td><td>--</td></tr><tr><td>C. elegans (Stony Brook)</td><td>C31A11.6</td><td>--</td><td>Caenorhabditis elegans cosmid C31A11, complete sequence</td><td>42,78%</td></tr></table>		gene	locus	description	%similarity to human	mouse (MGD)	Ccr4	9 (61.00 cM)	chemokine (C-C motif) receptor 4	--	C. elegans (Stony Brook)	C31A11.6	--	Caenorhabditis elegans cosmid C31A11, complete sequence	42,78%
	gene	locus	description	%similarity to human												
mouse (MGD)	Ccr4	9 (61.00 cM)	chemokine (C-C motif) receptor 4	--												
C. elegans (Stony Brook)	C31A11.6	--	Caenorhabditis elegans cosmid C31A11, complete sequence	42,78%												
SNPs/Variants (According to the NCBI SNP Database and to SWISS-PROT)	Variants: SWISS-PROT: CKR4 HUMAN NCBI SNPs: All NCBI SNPs in CCR4															
Disorders & Mutations (in which this Gene is Involved, According to OMIM , SWISS-PROT , Genatlas , GeneClinics , HGMD , BCGD , and/or TGDB .)	--															
Medical News (Possibly Related Articles in Doctor's Guide)	--															
Research Articles (in PubMed)	<ul style="list-style-type: none">• Molecular cloning and functional expression of a novel CC chemokine receptor cDNA from basophilic cell line.• The genes encoding the human CC-chemokine receptors CC-CKR1 to CC-CKR5 (CCL1 to CCL5) clustered in the p21.3-p24 region of chromosome 3.• New variations of human CC-chemokine receptors CCR3 and CCR4. <div><input type="text" value="Search PubMed for CCR4"/> to find abstracts of research articles containing th</div>															
CCR4 in Other Genome Wide Resources: (According to GDB , LocusLink , euGenes , Ensembl and/or GeneLynx)	GDB: 677463 LocusLink: 1233 euGenes: HUgn1233 GeneLynx: 2211															
CCR4 in General Databases, Limited Scope (According to HUGE)	--															
CCR4 in Specialized Databases (According to ATLAS , GENATLAS , HORDE , IMGT , MTDB , LEIDEN and/or SWISS-PROT)	name GenAtlas biochemistry entry for CCR4: chemokine CC,beta,receptor 4,with high affinity binding for basophil chemoattractant,G protein coupled receptor superfamily,specific receptor for thymus and activation-regulated chemokine			description Links to sequences , lin and papers												
Services (According to RZPD)	--															
<div>Back (to Search Results) - More like this</div>																

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The GeneCards **idea** in brief: [Mining the Internet](#) for biomedical knowledge and [guiding the user](#) to it.

Developed at the [Crown Human Genome Center & Weizmann Institute of Science](#)

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GeneCard for gene **CCL17**
GC16P047843

Approved UCL/HGNC/HUGO Human Gene Nomenclature database symbol
CCL17 (chemokine (C-C motif) ligand 17)

**Aliases and
Additional
Descriptions**
(According to GDB,
HUGO, and/or
SWISS-PROT)

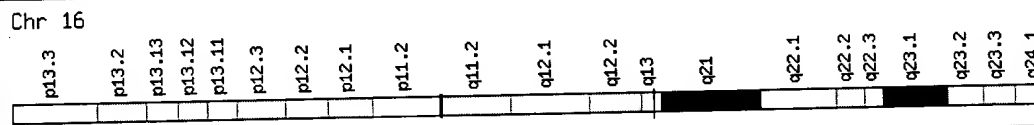
- A-152E5.3
- ABCD-2
- SCYA17
- **TARC**
- Human mRNA for chemokine, complete cds
- chemokine (C-C motif) ligand 17
- small inducible cytokine subfamily A (Cys-Cys), member 17
- Small inducible cytokine A17 precursor (CCL17) (Thymus and activation- regulated ch

**Chromosomal
Location**
(According to
UDB/GeneLoc and/or
HUGO, and/or
LocusLink,
Genomic Views
According to UCSC
and Ensembl)

Chromosome: 16 UDB/GeneLoc gene densities

LocusLink cytogenetic band: **16q13** Ensembl cytogenetic band: **16q13**

Gene in genomic location: bands according to Ensembl, locations according to UDB/GeneLoc



Unified DataBase (GeneLoc) location for GC16P047843: (about GC identifiers)

Start: 47,843,154 bp from pter

End: 47,845,335 bp from pter

Size: 2,181 bases

Orientation: plus strand

Unified DataBase (version 2.5) coordinate (from pter): --

Genomic View:
UCSC Golden Path

Proteins
(According to
SWISS-PROT and/or
MIPS)

SY17 HUMAN

- **Size:** 94 amino acids; 10507 Da
- **Function:** CHEMOTACTIC FACTOR FOR T LYMPHOCYTES BUT NOT MONOCYTE IN T CELL DEVELOPMENT IN THYMUS AND IN TRAFFICKING AND ACTIVATION (AND CCR8.
- **Subcellular location:** Secreted.
- **Tissue specificity:** EXPRESSED AT HIGH LEVELS IN THYMUS AND AT LOW LEVE SMALL INTESTINE.
- **Induction:** BY PHYTOHEMAGGLUTININ (PHA) IN THE PERIPHERAL BLOOD MONI IN MONOCYTES.
- **Similarity:** BELONGS TO THE INTERCRINE BETA FAMILY (SMALL CYTOKINE C-C

MIPS Pedant Viewer: 13657

REFSEQ proteins: NP_002978.1

InterPro Domains and Families:

**Protein Domains/
Families/Ontologies**
(According to InterPro,
GO, and/or BLOCKS)

IPR000827; CC chemkine sm1
IPR001811; Chemokine IL8

Graphical View of Domain Structure for SP Entry Q92583

Gene Ontology (GO) terms (tree view):

GO:0006935
GO:0007267
GO:0005576
GO:0006954
GO:0006955
GO:0007186
GO:0007275
GO:0008009

Blocks protein family: IPB000827 Small cytokines (intercrine/chemokine)

Sequences
(GenBank/EMBL/DDBJ
Accessions According
to Unigene or
GenBank, RefSeq
According to
LocusLink, Assembly
According to MIPS
and/or DOTS)

REFSEQ mRNAs: NM_002987.2

Additional Gene/cDNA sequence:
AC004382.1 BE061171.1 D43767 D43767.1

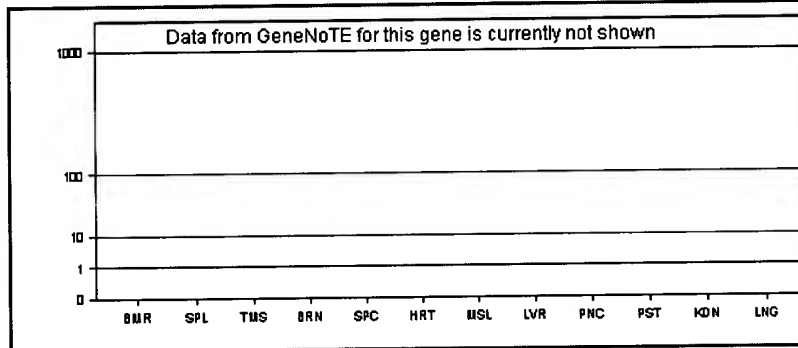
MIPS assembly: H9978S1

Unigene Cluster for CCL17: (Build 155 Homo sapiens; Sep 23 2002)
chemokine (C-C motif) ligand 17
Hs.66742

Unigene Representative Sequence: NM_002987

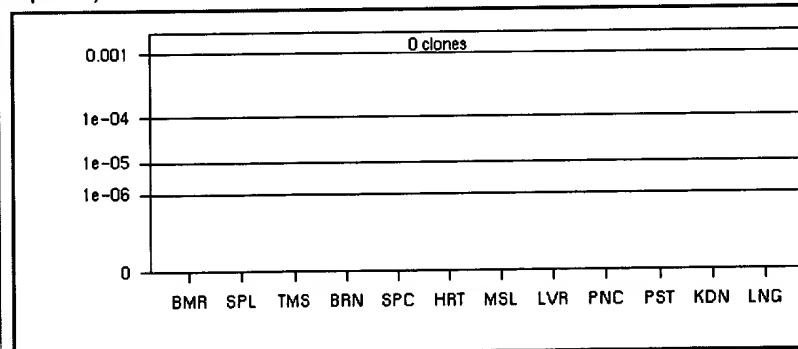
**Expression
in Human Tissues**
(According to
proprietary W.I.S DNA
array results
(GeneNoTE), UniGene
and/or SOURCE)

CCL17 expression in normal human tissues based on proprietary W.I.S DNA array (GeneNoTE)



- ☒ Immune System
- ☒ Nervous System
- ☐ Muscle
- ☒ Secretory Glands
- ☒ Other
- ☐ Min-max range for

CCL17 expression in normal human tissues based on quantifying ESTs from various sapiens).



- Tissue**
- BMR Bone marrow
 - SPL Spleen
 - TMS Thymus
 - BRN Brain
 - SPC Spinal cord
 - Heart
 - Skeletal muscle
 - LVR Liver
 - PNC Pancreas
 - PST Prostate
 - KDN Kidney
 - LNG Lung

SOURCE GeneReport for Unigene cluster Hs.66742

Similar Genes in Other Organisms (According to MGD Oct 16 2002 , Stony Brook C.elegans-H.sapiens Alignment Database and/or euGenes)	Homologues: <table><tr><td></td><td>gene</td><td>locus</td><td></td><td>description</td><td>%similarity to human</td><td colspan="2">GenBank accession</td></tr><tr><td>mouse (MGD)</td><td>Ccl17</td><td>8 (45.00 cM)</td><td></td><td>chemokine (C-C motif) ligand 17</td><td>--</td><td colspan="2">AF125570 AF125571 AK007663 BC028</td></tr></table>								gene	locus		description	%similarity to human	GenBank accession		mouse (MGD)	Ccl17	8 (45.00 cM)		chemokine (C-C motif) ligand 17	--	AF125570 AF125571 AK007663 BC028	
	gene	locus		description	%similarity to human	GenBank accession																	
mouse (MGD)	Ccl17	8 (45.00 cM)		chemokine (C-C motif) ligand 17	--	AF125570 AF125571 AK007663 BC028																	
SNPs/Variants (According to theNCBI SNP Database and to SWISS-PROT)	Variants: <u>SWISS-PROT</u> : SY17 <u>HUMAN</u>																						
	NCBI SNPs: 3 selected, not withdrawn, single nucleotide mutations are shown here.																						
	Genomic Data																						
	SNP ID	Contig Accession	Pos in Contig	Str	5' Flanking Sequence*	3' Flanking Sequence*	Validation	DN. Ch.															
	rs223828	NT_010463.10	637161	+	TCTGCCTGGT	GACTCCCCGA	by-frequency	C/T															
rs223827	NT_010463.10	635754	+	GTGCGAGGCC	ACCAAGGGGG	no-info	T/C																
rs1423768	NT_010463.10	635973	-	CCACCCCTCA	CAAGGGCTGC	no-info	G/T																
	* Lower case letters indicate repetitive or low-complexity sequence																						
	All NCBI SNPs in <u>CCL17</u>																						
Disorders & Mutations (in which this Gene is Involved, According to OMIM, SWISS-PROT, Genatlas, GeneClinics, HGMD, BCGD, and/or TGDB.)	--																						
Medical News (Possibly Related Articles in Doctor's Guide)	--																						
Research Articles (in PubMed)	<ul style="list-style-type: none">• Genome duplications and other features in 12 Mb of DNA sequence from human chromosome 16q11-13• Assignment of the human CC chemokine gene TARC (SCYA17) to chromosome 16q11-13• Molecular cloning of a novel T cell-directed CC chemokine expressed in thymus by signal transduction <div>Search PubMed for CCL17</div> to find abstracts of research articles containing TARC																						
CCL17 in Other Genome Wide Resources: (According to GDB, LocusLink, euGenes, Ensembl and/or GeneLynx)	<u>GDB: 4562685</u> <u>LocusLink: 6361</u> <u>euGenes: HUqn6361</u> <u>Ensembl: ENSG00000102</u>																						
CCL17 in General Databases, Limited Scope (According to HUGE)	--																						
CCL17 in Specialized Databases (According to ATLAS, GENATLAS, HORDE, IMGT, MTDB, LEIDEN and/or SWISS-PROT)	--																						

Services
(According to [RZPD](#))

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Developed at the [Crown Human Genome Center & Weizmann Institute of Science](#)

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